# WEST Search History

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DATE: Monday, October 17, 2005

| Hide? | Set Name | Query | Hit Count |
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| | *DB=PGPB,USPT; THES=ASSIGNEE; PLUR=YES; OP=ADJ* | | |
| ☐ | L1 | lipase | 20084 |
| ☐ | L2 | L1 and senescence | 324 |
| ☐ | L3 | L2 and transgenic | 188 |
| ☐ | L4 | L3 and plant | 164 |

END OF SEARCH HISTORY

10/674,540

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| | | |
|---|---|---|
| NEWS 1 | | Web Page URLs for STN Seminar Schedule - N. America |
| NEWS 2 | | "Ask CAS" for self-help around the clock |
| NEWS 3 | JUL 20 | Powerful new interactive analysis and visualization software, STN AnaVist, now available |
| NEWS 4 | AUG 11 | STN AnaVist workshops to be held in North America |
| NEWS 5 | AUG 30 | CA/CAplus -Increased access to 19th century research documents |
| NEWS 6 | AUG 30 | CASREACT - Enhanced with displayable reaction conditions |
| NEWS 7 | SEP 09 | ACD predicted properties enhanced in REGISTRY/ZREGISTRY |
| NEWS 8 | OCT 03 | MATHDI removed from STN |
| NEWS 9 | OCT 04 | CA/CAplus-Canadian Intellectual Property Office (CIPO) added to core patent offices |
| NEWS 10 | OCT 06 | STN AnaVist workshops to be held in North America |
| NEWS 11 | OCT 13 | New CAS Information Use Policies Effective October 17, 2005 |
| NEWS 12 | OCT 17 | STN(R) AnaVist(TM), Version 1.01, allows the export/download of CAplus documents for use in third-party analysis and visualization tools |

| | |
|---|---|
| NEWS EXPRESS | JUNE 13 CURRENT WINDOWS VERSION IS V8.0, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 13 JUNE 2005 |
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| NEWS INTER | General Internet Information |
| NEWS LOGIN | Welcome Banner and News Items |
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* * * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 18:20:23 ON 17 OCT 2005

=> file agricola biosis caplus

| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
|---|---|---|
| FULL ESTIMATED COST | 0.21 | 0.21 |

FILE 'AGRICOLA' ENTERED AT 18:20:46 ON 17 OCT 2005

FILE 'BIOSIS' ENTERED AT 18:20:46 ON 17 OCT 2005


FILE 'CAPLUS' ENTERED AT 18:20:46 ON 17 OCT 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

```
=> s lipase
L1       85115 LIPASE

=> l1 and senescence
L1 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s l1 and senescence
L2         190 L1 AND SENESCENCE

=> s l2 and (transgenic or transform?)
L3          14 L2 AND (TRANSGENIC OR TRANSFORM?)

=> d his

     (FILE 'HOME' ENTERED AT 18:20:23 ON 17 OCT 2005)

     FILE 'AGRICOLA, BIOSIS, CAPLUS' ENTERED AT 18:20:46 ON 17 OCT 2005
L1        85115 S LIPASE
L2          190 S L1 AND SENESCENCE
L3           14 S L2 AND (TRANSGENIC OR TRANSFORM?)

=> d ti

L3   ANSWER 1 OF 14  AGRICOLA  Compiled and distributed by the National
     Agricultural Library of the Department of Agriculture of the United States
     of America.  It contains copyrighted materials.  All rights reserved.
     (2005) on STN
TI   Altered membrane lipase expression delays leaf
     senescence.


=> dup rem l3
PROCESSING COMPLETED FOR L3
L4           12 DUP REM L3 (2 DUPLICATES REMOVED)

=> d ab l4

L4   ANSWER 1 OF 12  CAPLUS  COPYRIGHT 2005 ACS on STN
AB   Identification of blood-based biomarkers with predictive power in
     directing clin. outcomes is an active area of clin. research.  Methods are
     provided for determining whether a subject has a graft tolerant phenotype.
     Global gene expression monitoring is used to test whether blood-based
     markers for diagnostic of spontaneously achieved tolerance could be
     identified in a cohort of long-term renal transplant patients.  By
     normalizing to the average expression levels in normal control blood samples,
     several functional groups of genes were identified to be at significantly
     higher levels in the tolerant patients, where the identified genes
     included genes characteristic of rapid cell proliferation, anti-apoptotic
     activity and senescence, as well as genes involved in immune
     signaling cascades including specific transcription factors, cell adhesion
     mols.  Overall the data shows that the spontaneously achieved state of
     immunetolerance is an active regulatory process as evidenced by the large
     nos. of up-regulated genes relative to normal blood and by the highly
     synchronized expression signature that is observed  The methods and compns.
     find use in a variety of applications, including the determination of an
     immunosuppressive therapy regimen.


=> d l4 ab 1-12

L4   ANSWER 1 OF 12  CAPLUS  COPYRIGHT 2005 ACS on STN
AB   Identification of blood-based biomarkers with predictive power in
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Global gene expression monitoring is used to test whether blood-based markers for diagnostic of spontaneously achieved tolerance could be identified in a cohort of long-term renal transplant patients. By normalizing to the average expression levels in normal control blood samples, several functional groups of genes were identified to be at significantly higher levels in the tolerant patients, where the identified genes included genes characteristic of rapid cell proliferation, anti-apoptotic activity and **senescence**, as well as genes involved in immune signaling cascades including specific transcription factors, cell adhesion mols. Overall the data shows that the spontaneously achieved state of immunetolerance is an active regulatory process as evidenced by the large nos. of up-regulated genes relative to normal blood and by the highly synchronized expression signature that is observed The methods and compns. find use in a variety of applications, including the determination of an immunosuppressive therapy regimen.

L4 ANSWER 2 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN
AB The present invention provides methods for diagnosing mental disorders (e.g., psychotic disorders such as schizophrenia). The present invention uses DNA microarray anal. to demonstrate differential expression of genes in selected regions of post-mortem brains from patients diagnosed with mental disorders in comparison with normal control subjects. The invention also provides methods of identifying modulators of such mental disorders as well as methods of using these modulators to treat patients suffering from such mental disorders.

L4 ANSWER 3 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN
AB Regulation of expression of **senescence** in plants is achieved by integration of a gene or gene fragment encoding **senescence** -induced **lipase** into the plant genome in antisense orientation. The carnation and Arabidopsis genes encoding **senescence**-induced **lipase** are identified and the nucleotide sequences are used to modify **senescence** in **transgenic** plants.

L4 ANSWER 4 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN
AB This invention provides reagents and methods for identifying genes whose expression is modulated by induction of CDK inhibitor gene expression. The invention also provides reagents and methods for identifying compds. that inhibit the effects of CDK inhibitors such as p21, p27 and p16 on cellular gene expression, as a first step in rational drug design for preventing pathogenic consequences of cellular **senescence**, such as carcinogenesis and age-related diseases.

L4 ANSWER 5 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN
AB Regulation of expression of **senescence** in plants is achieved by integration of a gene or gene fragment encoding **senescence** -induced **lipase** into the plant genome in antisense orientation. This results in inhibition of **senescence**-induced **lipase** gene which increases resistance of plants to environmental stress-induced **senescence**, enhanced biomass of the plant and increased seed yield. This method has been applied to fruit-bearing plants, flowering plants, vegetables, agronomic crop plants and forest species. The carnation and Arabidopsis genes encoding **senescence**-induced **lipase** are identified and the nucleotide sequences are used to modify **senescence** in **transgenic** plants.

L4 ANSWER 6 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN
AB The invention discloses methods, gene databases, gene arrays, protein arrays, and devices that may be used to determine the hypersensitivity of individuals to a given agent, such as drug or other chemical, in order to prevent toxic side effects. In one embodiment, methods of identifying hypersensitivity in a subject by obtaining a gene expression profile of multiple genes associated with hypersensitivity of the subject suspected to be hypersensitive, and identifying in the gene expression profile of the subject a pattern of gene expression of the genes associated with hypersensitivity are disclosed. The gene expression profile of the subject may be compared with the gene expression profile of a normal individual and a hypersensitive individual. The gene expression profile of the subject that is obtained may comprise a profile of levels of mRNA

or cDNA. The gene expression profile may be obtained by using an array of nucleic acid probes for the plurality of genes associated with hypersensitivity. The expression of the genes predetd. to be associated with hypersensitivity is directly related to prevention or repair of toxic damage at the tissue, organ or system level. Gene databases arrays and apparatus useful for identifying hypersensitivity in a subject are also disclosed.

L4 ANSWER 7 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN
AB Chlorophyllase from Chenopodium album and Arabidopsis thaliana, and cDNAs, and **transgenic** plants **transformed** with them, are disclosed. Chlorophyllase (Chlase) is the first enzyme involved in chlorophyll (Chl) degradation and catalyzes the hydrolysis of ester bond to yield chlorophyllide and phytol. In the present study, we isolated the Chlase cDNA. We synthesized degenerate oligo DNA probes based on the internal amino acid sequences of purified Chlase from Chenopodium album, screened the C. album cDNA library, and cloned a cDNA (CaCLH, C. album chlorophyll-chlorophyllido hydrolase). The deduced amino acid sequence (347 aa residues) had a **lipase** motif overlapping with an ATP/GTP-binding motif (P-loop). CaCLH possibly was localized in the extraplastidic part of the cell, because a putative signal sequence for endoplasmic reticulum is at the N terminus. The amino acid sequence shared 37% identity with a function-unknown gene whose mRNA is inducible by coronatine and methyljasmonate (MeJA) in Arabidopsis thaliana (AtCLH1). We expressed the gene products of AtCLH1 and of CaCLH in Escherichia coli, and they similarly exhibited Chlase activity. Moreover, we isolated another full-length cDNA based on an Arabidopsis genomic fragment and expressed it in E. coli, demonstrating the presence of the second Arabidopsis CLH gene (AtCLH2). No typical feature of signal sequence was identified in AtCLH1, whereas AtCLH2 had a typical signal sequence for chloroplast. AtCLH1 mRNA was induced rapidly by a treatment of MeJA, which is known to promote **senescence** and Chl degradation in plants, and a high mRNA level was maintained up to 9 h. AtCLH2, however, did not respond to MeJA.

L4 ANSWER 8 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN
AB Regulation of expression of **senescence** in plants is achieved by integration of a gene or gene fragment encoding **senescence** -induced **lipase** into the plant genome in antisense orientation. The carnation gene encoding **senescence**-induced **lipase** is identified and the nucleotide sequence is used to modify **senescence** in **transgenic** plants.

L4 ANSWER 9 OF 12 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2005) on STN DUPLICATE 1

L4 ANSWER 10 OF 12 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
AB When studying the **senescence** of lupine, soybean and bean nodules, special attention was paid to structural and functional organization of the nitrogen-fixing symbiotic system and specifics of pro- and eukaryotic cell relationships. It was shown that changes in the ultrastructure of macrosymbiont (a decrease in ribosome number, vesiculation of granular endoplasmic reticulum and Golgi apparatus dictyosomes, mitochondrial swelling, and nucleoplasma clarification) and microsymbiont (increased peribacteroid space (PBS) volume, symbiosome fusion, bacteroid lysis) took place during aging. Experiments proved that during **senescence**, PBS became a lytic compartment exhibiting acid phosphatase and **lipase** activities. The enzymes entered PBS by fusion of primary lysosomes with peribacteroid membrane. At the same time, symbiosome **transformed** into secondary lysosome where bacteroid lysis took place. During effective symbiosis, nodule **senescence** in many legumes took place at the end of the reproductive phase. In noneffective nodules (plant infection with Rhizobium), bacteria did not **transform** into bacteroids and quickly aged in the infected cells. Abnormal symbiosome structure was observed during this process as was degradation of plant cell immature

bacteroids and organelles. Drought, hypoxia, darkness and high calcium doses accelerated nodule **senescence**. Rhizobium leguminosarum and Bradyrhizobium lupini were used for seed inoculation.

L4 ANSWER 11 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN
AB **Senescence** of lupine, soybean, and broad bean nodules was studied with emphasis on the structural and functional organization of the symbiotic tissue and specific interrelations between pro- and eukaryotic cells. Some **senescence**-related changes were observed in the ultrastructure of both macrosymbiont (a decrease in the number of ribosomes, vesicle formation from granular endoplasmic reticulum and Golgi dictyosomes, mitochondria swelling, and nucleoplasm lightening) and microsymbiont (an increase in the volume of the peribacteroid space (PBS), a symbiosome fusion, and a lysis of bacteroids). The PBS was exptl. shown to become a lytic compartment during nodule **senescence**, with the activities of acid phosphatase and **lipase** within it. These enzymes entered into the PBS from primary lysosomes after peribacteroid and lysosome membranes were fused. As a result, symbiosomes were **transformed** into secondary lysosomes exerting a bacteroid lysis. Nodule **senescence** in many legumes inoculated with effective rhizobium strains commenced by the end of the reproductive phase. In ineffective nodules (inoculation with fix- rhizobia), bacteria in infected cells failed to **transform** into bacteroids and senesced very rapidly. In this case, symbiosomes had an anomalous structure, and undeveloped bacteroids and plant cell organelles degraded. Some unfavorable environmental factors (drought, hypoxia, darkness, calcium excess) accelerated nodule **senescence**.

L4 ANSWER 12 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN
AB Aged mice exhibit an increase in their body weight (BW), which is associated with fat deposit increase. Epidermal growth factor (EGF) concentration in the submandibular gland also increases with aging. The authors examined the effects of elevated EGF on the adiposity of aged female mice. Studies were started in two groups of animals consisting of sham-operated and sialoadenectomized (Sx; surgical removal of the submandibular glands) mice at 8 wk of age. Body weight gain and food intake were measured throughout 78 wk of age in these two groups. Body weight was significantly less in the Sx group throughout 78 wk, while food intake was not changed by Sx after 12 wk of age. To examine further if EGF plays a role in the induction of adiposity in aged female mice, sham-operated animals were given 100 μl anti-EGF rabbit antiserum (anti-EGF group) or normal rabbit serum (control group) every 3 days, and Sx animals were given 5 μg/day EGF (Sx + EGF group) or saline (Sx group) from 78 wk of age for 3 wk. At 81 wk of age, all animals of these four groups were killed, and carcass fat deposition and fat cell sizes were measured. Although the relative wts. (weight ratio to BW) of the liver and kidney were not changed by Sx and anti-EGF treatment, the relative wts. of mesenteric and s.c. fat tissues and adipocyte wts. were significantly decreased in Sx and anti-EGF groups compared with the control group. Moreover, both acyl-CoA synthetase (ACS) and lipoprotein **lipase** (LPL) mRNA levels were significantly decreased by Sx or anti-EGF administration in mesenteric and s.c. fat tissues. EGF administration to Sx animals had no effect on BW, fat tissues and adipocyte wts., and ACS and LPL mRNA levels. The results, however, were consistent with the fact that adipose tissue EGF receptors were down regulated in Sx mice. These findings suggest that EGF may play a role in the induction of adiposity in aged female mice.